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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Huston, James S
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Cohen, Charles M
Crea, Roberto
Keck, Peter C
Oppermann, Hermann
Rueger, David C
Ridge, Richard J

(ii) TITLE OF INVENTION: Product and Process for the Production, Isolation and Purification of Recombinant Polypeptides

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Hopkinton
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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/661,070
(B) FILING DATE: 26-FEB-1991
(C) CLASSIFICATION: 435/68
536/27
530/300
530/350

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lunn, Paul G.
(B) REGISTRATION NUMBER: 32,743
(C) REFERENCE/DOCKET NUMBER: CRP-008DV

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (508) 435-9001
(B) TELEFAX: (508) 435-6951

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Glu Gly Arg
1

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GCT AAA AAC CTT AAC GAA GCT                                          21
Ala Lys Asn Leu Asn Glu Ala
  1               5
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Lys Asn Leu Asn Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
1 5 10 15

Ser Arg Leu Asp Leu Asp Val Arg Thr Asp His Lys Asp Leu Ser Asp
20 25 30

His Leu Val Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Val
35 40 45

Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Glu
50 55

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Phe Met Arg
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Phe Asp Pro Pro Pro Lys Phe Met Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Phe Asp Pro Pro Pro Met Pro Arg Lys Phe Met Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Phe Asp Pro Pro Pro Met Pro Arg Met Pro Asp Pro Glu Leu Arg
1 5 10 15

Lys Phe Met Arg
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
1 5 10 15

Ser Arg Ile Glu Leu Glu Met Arg Thr Asp His Lys Glu Leu Ser Glu
20 25 30

His Leu Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Cys

```
                35                  40                  45

Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Thr Lys Val Asp Arg Tyr
    50                  55                  60

Ser Tyr Val Met His Leu Val Ser Arg Val Val Gly Glu Leu Arg His
65                  70                  75                  80

Asp Leu Asp Ala Leu His Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
                85                  90                  95

Leu Ser Gly Ala Pro Lys Val Arg Ala Met Gln Leu Ile Ala Glu Ala
            100                 105                 110

Glu Gly Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Phe Thr
        115                 120                 125

Ala His Gly Asp Leu Asp Thr Cys Ile Val Ile Arg Ser Ala Leu Val
    130                 135                 140

Glu Asn Gly Ile Ala Thr Val Gln Ala Gly Ala Gly Val Val Leu Asp
145                 150                 155                 160

Ser Val Pro Gln Ser Glu Ala Asp Glu Thr Arg Asn Lys Ala Arg Ala
                165                 170                 175

Val Leu Arg Ala Ile Ala Thr Ala His His Ala Gln Glu Phe Pro Gly
            180                 185                 190

Glu
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
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```
372       1               5                   10                  15
373
374       Ser Arg Leu Asp Leu Asp Val Arg Thr Asp His Lys Asp Leu Ser Asp
375                   20                  25                  30
376
377       His Leu Val Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Val
378               35                  40                  45
379
380       Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Glu
381           50                  55
382
383   (2) INFORMATION FOR SEQ ID NO:13:
384
385        (i) SEQUENCE CHARACTERISTICS:
386             (A) LENGTH: 21 amino acids
387             (B) TYPE: amino acid
388             (C) STRANDEDNESS: single
389             (D) TOPOLOGY: linear
390
391       (ii) MOLECULE TYPE: peptide
392
393      (iii) HYPOTHETICAL: NO
394
395       (iv) ANTI-SENSE: NO
396
397        (v) FRAGMENT TYPE: internal
398
399
400
401       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
402
403        Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
404        1               5                   10                  15
405
406        Phe Met Pro Pro Cys
407                   20
408
409   (2) INFORMATION FOR SEQ ID NO:14:
410
411        (i) SEQUENCE CHARACTERISTICS:
412             (A) LENGTH: 19 amino acids
413             (B) TYPE: amino acid
414             (C) STRANDEDNESS: single
415             (D) TOPOLOGY: linear
416
417       (ii) MOLECULE TYPE: peptide
418
419      (iii) HYPOTHETICAL: NO
420
421       (iv) ANTI-SENSE: NO
422
423        (v) FRAGMENT TYPE: internal
424
```

425
426
427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
428
429 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
430 1 5 10 15
431
432 Phe Met Cys
433

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/661,070

DATE: 04/22/91
TIME: 09:27:54

LINE	ERROR	ORIGINAL TEXT
35	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/661,070
36	Wrong Filing Date	(B) FILING DATE: 26-FEB-1991
37	Wrong Classification	(C) CLASSIFICATION: 435/68

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/661,070

DATE: 04/22/91
TIME: 09:27:54

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/661,070

DATE: 04/22/91
TIME: 09:27:54

LINE	ORIGINAL TEXT	CORRECTED TEXT